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OM protein - protein search, using sw model

Run on: November 1, 2005, 18:53:46 ; Search time 163 Seconds
(without alignments)
35.591 Million cell updates/sec

Title: US-09-993-399-1

Perfect score: 79

Sequence: 1 RHYGETKMNQSRSS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	79	100.0	15	6	ABR61469 Human dis
2	79	100.0	355	8	ADG89869 Human kin
3	79	100.0	496	8	ADG89867 Human kin
4	79	100.0	2633	4	ABG06505 Novel hum
5	79	100.0	2863	4	AAM39097 Human pol
6	79	100.0	2663	8	ADQ17932 Human sof
7	79	100.0	2688	4	AAM40883 Human pol
8	69	87.3	2954	2	AAY01632 Amino aci
9	54	68.4	955	2	AAR57365 K39 polyp
10	54	68.4	955	2	AAR57365 K39 polyp
11	53	67.1	2013	4	AAM03691 Leishmani
12	52	65.8	154	3	ABb62322 Drosophil
13	52	65.8	154	3	ABb62322 Drosophil
14	52	65.8	341	5	ABb61636 Human ORF
15	52	65.8	341	5	ABb61636 Human str
16	52	65.8	341	5	ABb80079 Human kin
17	52	65.8	348	6	ABg72397 Human kin
18	52	65.8	1279	5	ABb80078 Human kin
19	52	65.8	1279	5	ABg70787 Human kin
20	52	65.8	1279	6	ABg72397 Human par
21	52	65.8	1401	7	ADJ94914 Novel NOV
22	51	64.6	726	3	ABb61012 Drosophil
23	51	64.6	829	3	AAG31118 Arabidops
24	51	64.6	834	3	AAG31116 Arabidops
25	-50	63.3	677	4	ABb65183 Drosophil

26	49	62.0	172	3	AAG14279 Arabidops
27	49	62.0	346	7	ADC23342 Human kin
28	49	62.0	346	8	ADQ60232 Human mic
29	49	62.0	346	8	ADQ60232 Human mic
30	49	62.0	370	7	ADC23338 Human kin
31	49	62.0	370	8	ADQ60228 Human mic
32	49	62.0	370	8	ADQ60228 Human mic
33	49	62.0	370	8	ADQ60228 Human mic
34	49	62.0	460	3	AA556650 Human pro
35	49	62.0	487	7	ADC23344 Human kin
36	49	62.0	487	8	ADQ60234 Human mic
37	49	62.0	487	8	ADQ60234 Human mic
38	49	62.0	490	7	ADK40973 Novel hum
39	49	62.0	490	8	ADK40973 Novel hum
40	49	62.0	512	7	ADC23340 Human kin
41	49	62.0	512	8	ADQ60230 Human mic
42	49	62.0	512	8	ADQ60230 Human mic
43	49	62.0	665	8	ADQ88355 Human KNS
44	48	60.8	324	2	AAW70235 Leishmani
45	48	60.8	324	5	AAE24949 Leishmani

ALIGNMENTS

RESULT 1

ABR61469

ID ABR61469 standard; peptide; 15 AA.

AC ABR61469;

DT 01-SEP-2003 (first entry)

DE Human disease specific marker CENP-E peptide.

KW Human; biopolymer marker; disease state; Alzheimer's disease.

OS Homo sapiens.

PN WO2003045992-A1.

PD 05-JUN-2003.

PF 31-OCT-2002; 2002WO-CA001646.

PR 23-NOV-2001; 2001US-00993399.

PA (SYNX-) SYN.X PHARMA INC.

PI Jackowski G, Marshall J;

DR WPI; 2003-505186/47.

PT New biopolymer marker, useful for indicating, determining risk-assessment of, or identifying therapeutic avenues related to, a disease state e.g., Alzheimer's disease.

PS Claim 1; Page 41; 44pp; English.

XX The invention relates to a novel biopolymer marker comprising a sequence having 13 amino acids or its analyte, useful in indicating at least one particular disease state. The biopolymer marker is useful for indicating, determining risk-assessment of, or identifying therapeutic avenues related to, a disease state e.g., Alzheimer's disease. The present sequence represents the biopolymer marker of the invention

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 6; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.1e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSRSS 15

```
Db      1 RHYGETKNQSSRS 15
|||||
RESULT 2
ADG89869
ID ADG89869 standard; protein; 355 AA.
XX
AC ADG89869;
XX
XX
DT 11-MAR-2004 (first entry)
DE
DE Human kinesin motor protein CENP-E340 SEQ ID NO:4.
KW human; CENP-E; HsCENP-E; kinesin motor protein; CENP-E340; cytostatic;
KW neuroprotective; gene therapy; cellular proliferation disorder; cancer;
KW neurological disorder; vesicular transport disorder;
KW hyperproliferative cell growth disorder; centromere-associated protein.
XX
OS Homo sapiens.
XX
PN WO2003104426-A2.
XX
XX
PD 18-DEC-2003.
XX
XX
PF 09-JUN-2003; 2003WO-US018203.
XX
XX
PR 10-JUN-2002; 2002US-0387403P.
XX
XX
PA (MERI ) MERCK & CO INC.
XX
PI Harvey DM, Yang Y, Kohl NE;
XX
DR WPI; 2004-062347/06.
DR N-PSDB; ADG89868.
XX
PT New centromere-associated motor protein, HsCENP-E, useful in diagnosing,
PT treating and preventing disorders characterized by excessive cellular
PT proliferation, including cancer, neurological disorders and disorders of
PT vesicular transport.
XX
PS Disclosure; SEQ ID NO 4; 108pp; English.
XX
CC The present sequence represents a human CENP-E (I) (HsCENP-E) which is a
CC kinesin motor protein, and a centromere-associated protein. The present
CC sequence is more specifically designated CENP-E340. Also described: (1) a
CC composition comprising (I) and a pharmaceutical excipient; (2) a method
CC for screening a compound as an agonist or antagonist of (I); (3) an
CC isolated and purified polynucleotide encoding (I), or which hybridises to
CC comprising the polynucleotide of (3); (6) a host cell comprising the
CC expression vector of (5); (7) a method for producing a polypeptide; (8) a
CC method of modulating cellular proliferation in a mammal; (9) a method of
CC inhibiting HsCENP-E mediated/induced cellular proliferation of a cell in
CC culture; and (10) a method of detecting the presence of cancer in an
CC individual. (I) has cytostatic and neuroprotective activities, and can be
CC used in gene therapy. The HsCENP-E protein can be used in screening
CC assays, in predictive medicine, e.g. diagnostic assays and
CC pharmacogenetics and in treating and preventing disorders characterised
CC by excessive cellular proliferation, including cancer, neurological
CC disorders and disorders of vesicular transport or useful in suppressing
CC hyperproliferative cell growth disorder.
XX
SQ Sequence 355 AA;
Query Match 100.0%; Score 79; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RHYGETKNQSSRS 15
|||||
Db      189 RHYGETKNQSSRS 203
|||||
RESULT 3
ADG89867
ID ADG89867 standard; protein; 496 AA.
XX
AC ADG89867;
XX
XX
DT 11-MAR-2004 (first entry)
DE
DE Human kinesin motor protein CENP-E465 SEQ ID NO:2.
KW human; CENP-E; HsCENP-E; kinesin motor protein; CENP-E465; cytostatic;
KW neuroprotective; gene therapy; cellular proliferation disorder; cancer;
KW neurological disorder; vesicular transport disorder;
KW hyperproliferative cell growth disorder; centromere-associated protein.
XX
OS Homo sapiens.
XX
PN WO2003104426-A2.
XX
XX
PD 18-DEC-2003.
XX
XX
PF 09-JUN-2003; 2003WO-US018203.
XX
XX
PR 10-JUN-2002; 2002US-0387403P.
XX
XX
PA (MERI ) MERCK & CO INC.
XX
PI Harvey DM, Yang Y, Kohl NE;
XX
DR WPI; 2004-062347/06.
DR N-PSDB; ADG89866.
XX
PT New centromere-associated motor protein, HsCENP-E, useful in diagnosing,
PT treating and preventing disorders characterized by excessive cellular
PT proliferation, including cancer, neurological disorders and disorders of
PT vesicular transport.
XX
PS Claim 1; SEQ ID NO 2; 108pp; English.
XX
CC The present sequence represents a human CENP-E (I) (HsCENP-E) which is a
CC kinesin motor protein, and a centromere-associated protein. The present
CC sequence is more specifically designated CENP-E465. Also described: (1) a
CC composition comprising (I) and a pharmaceutical excipient; (2) a method
CC for screening a compound as an agonist or antagonist of (I); (3) an
CC isolated and purified polynucleotide encoding (I), or which hybridises to
CC comprising the polynucleotide of (3); (6) a host cell comprising the
CC expression vector of (5); (7) a method for producing a polypeptide; (8) a
CC method of modulating cellular proliferation in a mammal; (9) a method of
CC inhibiting HsCENP-E mediated/induced cellular proliferation of a cell in
CC culture; and (10) a method of detecting the presence of cancer in an
CC individual. (I) has cytostatic and neuroprotective activities, and can be
CC used in gene therapy. The HsCENP-E protein can be used in screening
CC assays, in predictive medicine, e.g. diagnostic assays and
CC pharmacogenetics and in treating and preventing disorders characterised
CC by excessive cellular proliferation, including cancer, neurological
CC disorders and disorders of vesicular transport or useful in suppressing
CC hyperproliferative cell growth disorder.
XX
SQ Sequence 496 AA;
Query Match 100.0%; Score 79; DB 8; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RHYGETKNQSSRS 15
|||||
Db      189 RHYGETKNQSSRS 203
|||||
RESULT 4
ABG06505
```

ID ABG06505 standard; protein; 2633 AA.
 AC ABG06505;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #6496.
 XX
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
 KW
 KW
 KW
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US008631.
 PF
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 XX
 PI WPI; 2001-639362/73.
 XX N-PSDB; AAS70692.
 DR
 DR New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
 XX
 PT Claim 20; SEQ ID NO 36864; 103pp; English.
 PT
 PT The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pt_sequences
 XX
 SQ Sequence 2633 AA;
 Query Match 100.0%; Score 79; DB 4; Length 2633;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RHYGETKMQRRSSRS 15
 |||||
 Db 189 RHYGETKMQRRSSRS 203
 RESULT 5
 AAM39097
 ID AAM39097 standard; protein; 2663 AA.
 XX

AC AAM39097;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 2242.
 XX
 XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.
 KW
 KW
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 26-DEC-2000; 2000WO-US034263.
 PF
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-0052317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 PT Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI; 2001-442253/47.
 DR N-PSDB; AAI58253.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
 PT
 PS Example 4; SEQ ID NO 2242; 10078pp; English.
 XX
 XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
 XX
 SQ Sequence 2663 AA;
 Query Match 100.0%; Score 79; DB 4; Length 2663;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RHYGETKMQRRSSRS 15
 |||||
 Db 189 RHYGETKMQRRSSRS 203
 RESULT 6

ADQ17932
ID ADQ17932 standard; protein; 2663 AA.

XX AC ADQ17932;

XX DT 26-AUG-2004 (first entry)

XX DE Human soft tissue sarcoma-upregulated protein - SEQ ID 749.

XX KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.

XX OS Homo sapiens.

XX PN WO2004048938-A2.

XX PD 10-JUN-2004.

XX PF 26-NOV-2003; 2003WO-US038193.

XX PR 26-NOV-2002; 2002US-0429739P.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX PI Aziz N, Ginsburg WM, Zlotnik A;

XX DR WPI; 2004-441208/41.

XX PT Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue sarcoma.

XX PS Example 2; SEQ ID NO 749; 210pp; English.

XX CC The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.

XX SQ Sequence 2663 AA;

Query Match 100.0%; Score 79; DB 8; Length 2663;

Best Local Similarity 100.0%; Pred. NO. 0.00015; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 RHYGETKNQSSRS 15

XX Db 189 RHYGETKNQSSRS 203

RESULT 7

AAW40883

XX ID AAW40883 standard; protein; 2688 AA.

XX AC AAW40883;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 5814.

XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.

XX OS Homo sapiens.

XX PN WO200153312-A1.

XX PD 26-JUL-2001.

XX PF 26-DEC-2000; 2000WO-US034263.

XX PR 23-DEC-1999; 99US-00471275.

XX PR 21-JAN-2000; 2000US-00488725.

XX PR 25-APR-2000; 2000US-0052317.

XX PR 20-JUN-2000; 2000US-00598042.

XX PR 19-JUL-2000; 2000US-00620312.

XX PR 03-AUG-2000; 2000US-00653450.

XX PR 14-SEP-2000; 2000US-00662191.

XX PR 19-OCT-2000; 2000US-00693036.

XX PR 29-NOV-2000; 2000US-00727344.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;

XX PI Zhou P, Goodrich R, Drmanac RT;

XX DR WPI; 2001-442253/47.

XX DR N-PSDB; AAI60039.

XX PT Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

XX PS Example 2; SEQ ID NO 5814; 10078pp; English.

XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAI42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification

XX SQ Sequence 2688 AA;

Query Match 100.0%; Score 79; DB 4; Length 2688;

Best Local Similarity 100.0%; Pred. NO. 0.00015; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 RHYGETKNQSSRS 15

XX Db 213 RHYGETKNQSSRS 227

RESULT 8

AAAY01632

XX ID AAY01632 standard; protein; 2954 AA.

XX AC AAY01632;

XX DT 22-JUN-1999 (first entry)

XX DE Amino acid sequence of centromere-associated protein-E (CENP-E).

XX KW CENP-E; centromere-associated protein-E; ATPase activity;

KW plus end-directed microtubule motor activity; chromosome congression;
 KW microtubule binding activity; chromosome movement; mitosis;
 KW cell proliferation; tumor; metastasis; vascular malfunction;
 KW inflammatory disease; immune disease; angiogenesis; hypertension;
 KW restenosis; fungal infection; selective herbicide; fungicide;
 KW insecticide; plant growth regulator; activator; cancer cell marker.
 XX
 OS Xenopus sp.
 XX
 XX WO9913061-A1.
 PN
 XX
 PD 18-MAR-1999.
 XX
 XX
 PF 10-SEP-1998; 98WO-US019231.
 XX
 PR 11-SEP-1997; 97US-0058645P.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA
 FI Wood KW, Sakowicz R, Goldstein LSB, Cleveland DW;
 XX
 XX WPI; 1999-229233/19.
 DR
 DR N-PSDB; AAX26819.
 XX
 PT Centromere-associated protein-E and related nucleic acid.
 XX
 XX
 PS Claim 5; Page 66-67; 77pp; English.
 XX
 CC The present sequence represents CENP-E (centromere-associated protein-E)
 CC of Xenopus. The protein has at least one of plus end-directed microtubule
 CC motor activity, ATPase (adenosine triphosphatase) activity and
 CC microtubule binding activity. CENP-E is the motor that powers chromosome
 CC movement toward microtubule plus ends and is essential for congression of
 CC chromosomes during mitosis. Modulators of CENP-E can thus control cell
 CC proliferation. Agents that modulate CENP-E activity are lead therapeutic,
 CC bioagricultural and diagnostic agents, e.g. for treatment of unwanted
 CC cell proliferation (typical of many examples are tumors and metastases;
 CC vascular malfunction; inflammatory and immune diseases; angiogenesis;
 CC hypertension; restenosis; and fungal infections), also as plant-
 CC protection agents (selective herbicides, fungicides and insecticides) and
 CC plant growth regulators or activators for improving yields. CENP-E is
 CC also a diagnostic marker for dividing cells, including cancer cells
 XX
 XX Sequence 2954 AA;

Query Match 87.3%; Score 69; DB 2; Length 2954;
 Best Local Similarity 86.7%; Pred. No. 0.0099;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
 |||||
 Db 187 RHYGETKNQRRSSRS 201

RESULT 9
 AAR57365
 ID AAR57365 standard; protein; 955 AA.

XX
 XX AAR57365;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 08-MAR-1995 (first entry)
 XX
 XX
 DE K39 polypeptide of Leishmania chagasi.

XX Parasite; leishmaniasis; infection; repeat unit; vaccine; antigen;
 KW Leishmania chagasi.
 XX
 OS Leishmania donovani chagasi.
 XX
 PN WO9416331-A1.
 XX

PD 21-JUL-1994.
 XX
 XX 10-JAN-1994; 94WO-US000324.
 XX
 PR 15-JAN-1993; 93US-00006676.
 XX
 PA (IASY-) IASYS CORP.
 XX
 XX Reed SG;
 PI
 XX WPI; 1994-249402/30.
 DR
 DR N-PSDB; AAQ70152.
 XX
 PT Diagnosis of Leishmaniasis - by determining the presence of antibodies
 XX that bind to a K39 repeat unit antigen.
 PS Disclosure; Page 12-15; 28pp; English.
 XX

CC The K39 polypeptide comprises a number of repeated units (described in
 CC AAR57366). Detection of antibodies directed against this repeated unit in
 CC a patients sample is indicative of leishmaniasis. The antigenic repeat
 CC unit can itself be used as a vaccine to protect against infection by a
 CC leishmania parasite. (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 16-OCT-2003 to standardise OS field)
 XX
 XX Sequence 955 AA;

Query Match 68.4%; Score 54; DB 2; Length 955;
 Best Local Similarity 73.3%; Pred. No. 1.4;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
 |||||
 Db 241 RHYGETKNQRRSSRS 255

RESULT 10
 AAW03691
 ID AAW03691 standard; protein; 955 AA.

XX
 AC AAW03691;
 XX
 DT 16-OCT-2003 (revised)
 DT 09-MAR-1997 (first entry)
 XX
 XX Leishmania chagasi K39 antigen.
 DE
 XX Leishmania chagasi; acidic ribosomal antigen; LcP0; epitope; K39.
 KW
 XX Leishmania donovani chagasi.

OS
 XX WO9633414-A2.
 PN
 XX 24-OCT-1996.
 PD
 XX
 PF 19-APR-1996; 96WO-US005472.
 XX
 PR 21-APR-1995; 95US-00428414.
 XX
 XX (CORI-) CORIXA CORP.

XX
 XX Reed SG;
 PI
 XX WPI; 1996-485884/48.
 DR
 DR N-PSDB; AAT42166.
 XX

XX New Leishmania acidic ribosomal P-protein family poly:peptide - used to
 PT develop prods. for diagnosis, detection and protection against Leishmania
 PT infections.
 XX
 PS Disclosure; Page 36-43; 76pp; English.
 XX
 CC Compounds including polypeptides that contain at least an epitope of the

CC L. chagasi acidic ribosomal antigen Lcp0 are useful in a variety of
 CC immunoassays for detecting Leishmania infection. Portions of Lcp0
 CC (AA742164) contg. at least the 17 C-terminal amino acids (AA742165) have
 CC been found to generate a signal in an ELISA that is equivalent to that
 CC generated by the full length Lcp0. A combination polypeptide may also be
 CC used, comprising an Lcp0 epitope along with an epitope derived from the
 CC Leishmania K39 antigen (AA742166), pref. the K39 repeat unit antigen
 CC having the sequence given in AA03690. (Updated on 16-OCT-2003 to
 CC standardise OS field)
 XX
 XX Sequence 955 AA;

Query Match 68.4%; Score 54; DB 2; Length 955;
 Best Local Similarity 73.3%; Pred. No. 1.4;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 RHYGETKNQRRSSRS 15
 || |||| ||||
 DB 241 RHTASTKNDRSSRS 255

RESULT 11
 ABB62322
 ID ABB62322 standard; protein; 2013 AA.

AC ABB62322;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 13758.

XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US009231.

PR 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

DR WPI; 2001-656860/75.

DR N-PSDB; ABL06425.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.

PS Disclosure; SEQ ID NO 13758; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 2013 AA;

Query Match 67.1%; Score 53; DB 4; Length 1013;
 Best Local Similarity 73.3%; Pred. No. 4.6;

Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 RHYGETKNQRRSSRS 15
 || |||| ||||
 DB 183 RTVGETNNRRSSRS 197

RESULT 12

AAB40661
 ID AAB40661 standard; protein; 154 AA.

XX AAB40661;

DT 08-FEB-2001 (first entry)

DE Human ORFX ORF425 polypeptide sequence SEQ ID NO:850.

XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antineumatic; antithyroid;
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; hypothyroidism; SCID; AIDS;
 KW cardiovascular disease; diabetes mellitus; erythematous; infection;
 KW cholesterol ester storage; systemic lupus erythematosus; asthma;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; aschma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive.

XX Homo sapiens.

XX WO2000058473-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US008621.

XX 31-MAR-1999; 99US-0127607P.

XX 02-APR-1999; 99US-0127636P.

XX 05-APR-1999; 99US-0127728P.

XX 30-MAR-2000; 2000US-00540763.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2000-602362/57.

XX N-PSDB; AAC74870.

XX Novel nucleic acids and peptides derived from open reading frame X,

XX useful for treating e.g. cancers, proliferative disorders,

XX neurodegenerative disorders and cardiovascular disease.

XX Claim 11; Page 888-889; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
 CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
 CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
 CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
 CC antiviral; antifungal; antineumatic; antithyroid; and antianaemic. The
 CC sequences can be used for determining the presence of or predisposition
 CC to, or preventing or treating pathological conditions associated with an
 CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be
 CC used to treat cancers, proliferative disorders, neurodegenerative
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester

CC storage, systemic lupus erythematosus, severe combined immunodeficiency
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
 CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
 XX
 XX Sequence 154 AA;

Query Match 65.8%; Score 52; DB 3; Length 154;
 Best Local Similarity 66.7%; Pred. No. 0.42;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 RHVGTQNNQSSRS 15
 ||| ||| ||| |||
 Db 29 RHGTQNNHSSRS 43

RESULT 13
 ABP31636
 ID ABP31636 standard; protein; 154 AA.

AC ABP31636;

XX 09-JUL-2002 (first entry)

XX Human structural protein-like ORF609 protein, SEQ ID NO:1218.

KW Human; ORF; open reading frame; ORFX; drug screening; diagnosis;
 KW disease monitoring; cytokine; cell proliferation; cell differentiation;
 KW immune modulation; haematopoiesis regulation; tissue growth;
 KW angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
 KW behaviour; cancer; proliferative disorder; neurological disorder;
 KW cardiovascular disease; immune system disorder; organ transplantation;
 KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
 KW hypothyroidism; cholesterol ester storage disease; infection; vulnery;
 KW vasotropic; antipsoriatic; antidiabetic; cyrostatic; nootropic;
 KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
 KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
 KW dermatological; analgesic; virucide; antibacterial; fungicide.

XX Homo sapiens.

XX WO200190366-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US017076.

XX 24-MAY-2000; 2000US-0206690P.

XX (CURA-) CURAGEN CORP.

XX Leach MD, Shimkets RA;

XX WPI; 2002-106200/14.

XX N-PSDE; ABN75662.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and disorders related to organ
 PT transplantation.

XX Claim 10; Page 570; 2508pp; English.

XX Sequences ABP31028-ABP35561 represent 4534 novel human proteins
 CC designated ORP (open reading frame) 1-4534, and sequences ABN75054-
 CC ABN79587 represent cDNAs encoding them. The invention also encompasses
 CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
 CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
 CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
 CC polynucleotides, the recombinant production of ORFX proteins, antibodies
 CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and

CC polypeptides, methods of screening for modulators of ORFX expression or
 CC activity, and methods of screening individuals for a predisposition to an
 CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
 CC range of biological activities, such as cytokine, cell proliferation,
 CC cell differentiation, immune modulation, haematopoiesis regulation,
 CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
 CC chemokinetic activity, haemostatic activity, thrombolytic activity,
 CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
 CC and antiinfective activity, and may also be involved in the determination
 CC of bodily characteristics, fertility and behaviour. ORFX proteins, such
 CC as nucleic acids and antibodies may be used in the treatment of cancers,
 CC other proliferative disorders such as psoriasis and benign tumours,
 CC neurological disorders such as epilepsy and Alzheimer's disease,
 CC cardiovascular diseases, immune system disorders, disorders related to
 CC organ transplantation, disorders of tissue growth and regeneration,
 CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
 CC storage disease, and infectious diseases caused by viral, bacterial,
 CC fungal and other pathogens. ORFX nucleic acids may also be used as a
 CC source of primers and probes, in the detection of ORFX genomic sequences
 CC or transcripts, in the identification and cloning of homologous
 CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
 CC nucleic acids may additionally be used to produce transgenic animals
 CC which may be useful for studying the function and/or activity of ORFX
 CC protein, and in drug screening. The ORFX proteins may also be used as
 CC immunogens to generate specific antibodies, which are useful in the
 CC diagnosis, treatment and monitoring of ORFX-associated diseases
 XX

XX Sequence 154 AA;

Query Match 65.8%; Score 52; DB 5; Length 154;

Best Local Similarity 66.7%; Pred. No. 0.42;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 RHVGTQNNQSSRS 15

||| ||| ||| |||
 Db 29 RHGTQNNHSSRS 43

RESULT 14

ABB80079

ID ABB80079 standard; protein; 341 AA.

XX ABB80079;

XX 27-AUG-2002 (first entry)

XX Human kinesin motor protein (Hskrp5) motor domain amino acid sequence.

XX Human; kinesin motor protein; Hskrp5; cytostatic; cardiovascular;

XX immunomodulatory; anti-inflammatory; vaccine; gene therapy;

XX spindle morphogenesis; chromosome; cell division;

XX cellular proliferation disorder; cancer; hyperplasia; restenosis;

XX cardiac hypertrophy; immune disorder; inflammation.

XX Homo sapiens.

XX US6379941-B1.

XX 30-APR-2002.

XX 27-NOV-2000; 2000US-00724517.

XX 17-AUG-2000; 2000US-00641807.

XX (CYTO-) CYTOKINETICS INC.

XX Beraud C, Freedman R;

XX WPI; 2002-413719/44.

XX Isolated human Kinesin motor protein Hskrp5, useful for preventing,
 PT diagnosing and treating e.g. cancer, hyperplasia, restenosis, cardiac
 PT hypertrophy, immune disorders and inflammation.

XX Claim 4; Fig 4; 29pp; English.

PS The invention relates to an isolated human Kinesin motor protein

XX (HsKrp5). The activity of the protein of the invention may be described

CC as cytoskeletal, cardiovascular, immunomodulatory and anti-inflammatory.

CC The protein may be used in a vaccine or in gene therapy. Kinesin-related

CC proteins (KRPs) participate in spindle morphogenesis and chromosome

CC movement in cell division. The anti-HsKrp5 agonists, antibodies and

CC antagonists may be used to regulate HsKrp5 expression and activity. The

CC anti-HsKrp5 antibodies may also be used as diagnostic agents for

CC detecting the presence of HsKrp5 in samples (e.g. by enzyme linked

CC immunosorbent assay (ELISA)) and therefore diagnose diseases associated

CC with aberrant HsKrp5 expression and activity. They may be used in this

CC way to prevent, diagnose and treat cellular proliferation disorders e.g.

CC cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders

CC and inflammation. The current sequence represents the human kinesin motor

CC protein (HsKrp5) motor domain amino acid sequence

XX

SQ Sequence 341 AA;

Query Match 65.8%; Score 52; DB 5; Length 341;

Best Local Similarity 66.7%; Pred. No. 1;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSSRS 15

Db 192 RHTGTTQNHSSRS 206

RESULT 15

ABG72398

ID ABG72398 standard; protein; 341 AA.

AC ABG72398;

DT 11-FEB-2003 (first entry)

DE Human kinesin protein, HsKrp5, motor domain.

KW Human; kinesin; HsKrp5; ATPase; microtubule; cellular proliferation;

KW cancer; hyperplasia; restenosis; cardiac hypertrophy; autoimmune disease;

KW immune disorder; arthritis; graft rejection; inflammatory bowel disease;

KW inflammation; neurological disorder; vesicular transport disorder;

KW enzyme; motor domain.

OS Homo sapiens.

XX US6448026-B1.

XX 10-SEP-2002.

XX 27-NOV-2000; 2000US-00723096.

XX 17-AUG-2000; 2000US-00641807.

XX (CYTO-) CYTOKINETICS INC.

XX Beraud C, Freedman R;

XX WPI; 2003-089119/08.

XX N-PSDB; ABX13614.

XX Screening for modulators of human kinesin protein HsKrp5, which are

PT useful in treating cancers or restenosis, comprises detecting binding or

PT ATPase activity levels of the protein in a first and second concentration

PT of a candidate agent.

XX Claim 8; Fig 4; 30pp; English.

XX The invention relates to screening for modulators of a target protein,

CC comprises detecting the level of binding activity or ATPase activity of

CC the target protein when contacted with a first and second concentration

CC of a candidate agent. The target protein comprises a sequence that has

CC greater than 90% amino acid identity with a sequence of human kinesin

CC protein HsKrp5 (or its motor domain). The method is useful for screening

CC for modulators of a target protein having microtubule stimulated ATPase

CC activity, particularly the human kinesin protein HsKrp5. The modulators

CC of HsKrp5 are useful in diagnosing, preventing or treating cellular

CC proliferation (e.g. cancers (many examples given in the specification) or

CC hyperplasia), restenosis, cardiac hypertrophy, autoimmune disease, immune

CC disorders, arthritis, graft rejection, inflammatory bowel disease,

CC inflammation, neurological disorders, or disorders of vesicular

CC transport. The present sequence represents human HsKrp5, motor domain

XX

SQ Sequence 341 AA;

Query Match 65.8%; Score 52; DB 6; Length 341;

Best Local Similarity 66.7%; Pred. No. 1;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSSRS 15

Db 192 RHTGTTQNHSSRS 206

Search completed: November 1, 2005, 19:10:02

Job time : 166 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 1, 2005, 18:56:06 ; Search time 39 Seconds
(without alignments)
37.006 Million cell updates/sec

Title: US-09-993-399-1

Perfect score: 79

Sequence: 1 RHYGETKMNQSRSSRS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	2663	1 S28261	centromere protein
2	69	87.3	2954	2 T14156	kinesin-related pr
3	58	73.4	823	2 T52425	kinesin-like prote
4	58	73.4	888	2 D96619	protein T30516.9 [
5	54	68.4	955	2 A47334	LeKin kinesin-rela
6	51	64.6	581	2 F84599	probable kinesin h
7	51	64.6	834	2 T06055	hypothetical prote
8	50	63.3	1459	2 T30196	kinesin motor prot
9	49	62.0	198	2 E86183	hypothetical prote
10	49	62.0	665	2 S62328	kinesin-like DNA b
11	48	60.8	1070	2 T06733	kinesin homolog F2
12	47	59.5	670	2 T29898	kinesin protein OS
13	47	59.5	672	2 S54351	kinesin osm-3 - Ca
14	47	59.5	754	2 S48020	kinesin-related pr
15	47	59.5	733	2 S34830	kinesin-related pr
16	46	58.2	102	2 E85814	hypothetical prote
17	46	58.2	108	2 E90966	hypothetical prote
18	46	58.2	127	2 G64960	probable membrane
19	46	58.2	932	2 T49235	kinesin-like prote
20	45	57.0	143	2 C44259	kinesin heavy chai
21	45	57.0	315	2 AF1393	glycosyl transfera
22	45	57.0	315	2 A11768	glycosyl transfera
23	45	57.0	777	2 C85065	kinesin-like prote
24	45	57.0	963	1 A41919	kinesin heavy chai
25	45	57.0	967	1 A35075	kinesin heavy chai
26	45	57.0	975	1 A31497	kinesin heavy chai
27	45	57.0	1027	2 S37711	kinesin heavy chai
28	45	57.0	1031	1 A38713	kinesin heavy chai
29	45	57.0	1032	2 I38510	neuronal kinesin h

30 44 55.7 294 2 S38983 kinesin-related pr
31 44 55.7 706 1 C42640 kinesin-related pr
32 44 55.7 742 1 S58691 kinesin-related pr
33 44 55.7 987 2 B96766 protein kinesin F2
34 44 55.7 1130 2 T21134 hypothetical prote
35 43 54.4 332 2 C48835 kinesin-like prote
36 43 54.4 701 1 B44259 kinesin-related pr
37 43 54.4 747 1 A57107 kinesin-related pr
38 43 54.4 786 2 A53939 kinesin homolog KH
39 43 54.4 968 2 T45746 hypothetical prote
40 43 54.4 1056 2 C96661 kinesin-like prote
41 43 54.4 1263 2 T13465 hypothetical prote
42 42 53.2 699 1 S38982 kinesin-related pr
43 42 53.2 861 2 T00434 probable kinesin h
44 41 51.9 573 2 F72691 probable fumarate
45 41 51.9 770 1 A44337 kinesin-related pr

ALIGNMENTS

RESULT 1

S28261

centromere protein E - human

N;Alternate names: Centromere

C;Species: Homo sapiens (man)

C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004

C;Accession: S28261

R;Yen, T.J.; Li, G.; Schaar, B.T.; Szilak, I.; Cleveland, D.W.

Nature 359, 536-539, 1992

A;Title: CENP-E is a putative kinetochore motor that accumulates just before mitosis.

A;Reference number: S28261; MUID:93024922; PMID:1406971

A;Accession: S28261

A;Molecule type: mRNA

A;Residues: 1-2663 <YEN>

A;Cross-references: UNIPROT:Q02224; EMBL:Z15005; NID:G29864; PIDN:CAA78727.1; PID:G298

C;Genetics:

A;Gene: GDB:CEPNE

A;Cross-references: GDB:361164; OMIM:117143

A;Map position: 4q24-q25

C;Superfamily: centromere protein E; kinesin motor domain homology

C;Keywords: ATP; coiled coil; microtubule binding; mitosis; nucleotide binding; P-loop

F;7-335/Domain: kinesin motor domain homology <KMOT>

F;86-93/Region: nucleotide-binding motif A (P-loop)

F;486-2183/Domain: coiled coil #status predicted <COI>

F;92/Binding site: ATP (Lys) #status predicted

Query Match 100.0%; Score 79; DB 1; Length 2663;

Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYGETKMNQSRSSRS 15

Db 189 RHYGETKMNQSRSSRS 203

RESULT 2

T14156

kinesin-related protein - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T14156

R;Wood, K.W.; Sakowicz, R.; Goldstein, L.S.; Cleveland, D.W.

Cell 91, 357-366, 1997

A;Title: CENP-E is a plus end-directed kinetochore motor required for metaphase chromo:

A;Reference number: Z17893; MUID:98028574; PMID:9363944

A;Accession: T14156

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-2954 <WOO>

A;Cross-references: UNIPROT:O42263; EMBL:AF027728; NID:G2586070; PID:G2586071; PIDN:AA

C;Genetics:

A;Gene: KCENP-E

C;Superfamily: centromere protein E; kinesin motor domain homology

Query Match 87.3%; Score 69; DB 2; Length 2954;
Best Local Similarity 86.7%; Pred. No. 0.00076;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
|||||
Db 187 RHYGETKNQRRSSRS 201

RESULT 3

T52425

kinesin-like protein [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004

C;Accession: T52425

R;Kato, A.; Suzuki, M.; Kuwahara, A.; Ooe, H.; Higano-Inaba, K.; Kameda, Y.

Gene 239, 309-316, 1999

A;Title: Isolation and analysis of cDNA within a 300 kb Arabidopsis thaliana genomic region

A;Reference number: 225171

A;Accession: T52425

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-823 <KAT>

A;Cross-references: UNIPROT:Q9S7P3; EMBL:AB028468; PIDN:BAA88112.1

C;Genetics:

A;Gene: ZCF125

Query Match 73.4%; Score 58; DB 2; Length 823;
Best Local Similarity 73.3%; Pred. No. 0.021;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
|||||
Db 184 RHYGETKNQRRSSRS 198

RESULT 4

D96619

protein T30E16.9 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: D96619

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: D96619

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-888 <STO>

A;Cross-references: UNIPROT:Q9L062; GB:AE005173; NID:98778739; PIDN:AAF79747.1; GSPDB:GN

C;Genetics:

A;Gene: T30E16.9

A;Map position: 1

Query Match 73.4%; Score 58; DB 2; Length 888;
Best Local Similarity 73.3%; Pred. No. 0.023;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
|||||
Db 215 RHYGETKNQRRSSRS 229

RESULT 5

A47334

Lckin kinesin-related antigen - Leishmania chagasi (fragment)

C;Species: Leishmania chagasi

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A47334

R;Burns Jr., J.M.; Shreffler, W.G.; Benson, D.R.; Ghali, H.W.; Badaro, R.; Reed, S.G.

Proc. Natl. Acad. Sci. U.S.A. 90, 775-779, 1993

A;Title: Molecular characterization of a kinesin-related antigen of Leishmania chagasi

A;Reference number: A47334; MUID:93133867; PMID:8421715

A;Accession: A47334

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-955 <BUR>

A;Cross-references: UNIPROT:P46865; GB:L07879; NID:9308884; PIDN:AAA29254.1; PID:93088

A;Experimental source: MHOM/BR/82/BA-2.C1

A;Note: sequence extracted from NCBI backbone (NCBIN:122864, NCBIIP:122865)

C;Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology

C;Keywords: ATP; nucleotide binding; P-loop

F;13-398/Domain: kinesin motor domain homology <KMOT>

F;122-129/Region: nucleotide-binding motif A (P-loop)

Query Match 68.4%; Score 54; DB 2; Length 955;
Best Local Similarity 73.3%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
|||||
Db 241 RHYGETKNQRRSSRS 255

RESULT 6

F84599

probable kinesin heavy chain [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: F84599

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon,

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: F84599

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-581 <STO>

A;Cross-references: UNIPROT:Q9SJU7; GB:AE002093; NID:94567265; PIDN:AAD23678.1; GSPDB:

C;Genetics:

A;Gene: At2g21300

A;Map position: 2

Query Match 64.6%; Score 51; DB 2; Length 581;
Best Local Similarity 66.7%; Pred. No. 0.28;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
|||||
Db 205 RHYGETKNQRRSSRS 219

RESULT 7

T06055

hypothetical protein F19H22.50 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004

C;Accession: T06055

R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.

submitted to the Protein Sequence Database, March 1999

A;Reference number: 215184

A;Accession: T06055

A;Molecule type: DNA

A;Residues: 1-834 <BEV>

A;Cross-references: UNIPROT:Q9SVJ8; EMBL:AL035679; GSPDB:GN00062; ATSP:F19H22.50
 A;Experimental source: cultivar Columbia; BAC clone F19H22
 C;Genetics:

A;Gene: ATSP:F19H22.50

A;Map position: 4

A;Introns: 63/1; 93/1; 126/3; 164/3; 196/2; 234/3; 276/2; 389/3; 422/3; 633/3; 726/2
 C;Superfamily: kinesin heavy chain; kinesin motor domain homology
 F;14-339/Domain: kinesin motor domain homology <KMOT>

Query Match 64.6%; Score 51; DB 2; Length 834;

Best Local Similarity 66.7%; Pred. No. 0.41; 3; Indels 0; Gaps 0;

Matches 10; Conservative 2; Mismatches 0; Gaps 0;

Qy 1 RHYGETKMNQSSRS 15

||| ||| ||| ||| |||

Db 214 RKIGETSLNERSRS 228

RESULT 8

T30196

kinesin motor protein 1 - smut fungus (Ustilago maydis)

C;Species: Ustilago maydis (corn smut)

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C;Accession: T30196

R;Lehmler, C.; Steinberg, G.; Snetseelaar, K.M.; Schliwa, M.; Kahmann, R.; Bolker, M.

EMBO J. 16, 3464-3473, 1997

A;Title: Identification of a motor protein required for filamentous growth in Ustilago m

A;Reference number: 220770; MUID:97361828; PMID:9218789

A;Accession: T30196

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1459 <LEH>

A;Cross-references: UNIPROT:P87198; EMBL:U92844; NID:g2062749; PID:g2062750; PIDN:AAB633

C;Genetics:

A;Gene: kinl

C;Function:

A;Description: required for filamentous growth in Ustilago maydis

Query Match 63.3%; Score 50; DB 2; Length 1459;

Best Local Similarity 66.7%; Pred. No. 1.1; 4; Indels 0; Gaps 0;

Matches 10; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 RHYGETKMNQSSRS 15

||| ||| ||| ||| |||

Db 487 RHVGATDWNERSRS 501

RESULT 9

E86183

hypothetical protein [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: E86183

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: E86183

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-198 <STO>

A;Cross-references: UNIPROT:Q9MAU7; GB:A8005172; NID:g7211991; PIDN:AAP40462.1; GSPDB:GN

C;Genetics:

A;Map position: 1

Query Match 62.0%; Score 49; DB 2; Length 198;

Best Local Similarity 72.7%; Pred. No. 0.22; 1; Indels 0; Gaps 0;

Matches 8; Conservative 2; Mismatches 0; Gaps 0;

Qy 1 RHYGETKMNQSSRS 11

||| ||| ||| ||| |||

Db 73 RHYNETRINQSSRS 83

RESULT 10

S62328

kinesin-like DNA binding protein KID - human

C;Species: Homo sapiens (man)

C;Date: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 16-Aug-2004

C;Accession: S62328

R;Tokai, N.; Fujimoto-Nishiyama, A.; Toyoshima, Y.; Yonemura, S.; Tsukita, S.; Inoue,

EMBO J. 15, 457-467, 1996

A;Title: Kid, a novel kinesin-like DNA binding protein, is localized to chromosomes an

A;Reference number: S62328; MUID:96174806; PMID:8599929

A;Accession: S62328

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-665 <TOX>

C;Superfamily: kinesin motor domain homology

C;Keywords: ATP; nucleotide binding; P-loop

F;44-374/Domain: kinesin motor domain homology <KMOT>

F;128-135/Region: nucleotide-binding motif A (P-loop)

Query Match 62.0%; Score 49; DB 2; Length 665;

Best Local Similarity 66.7%; Pred. No. 0.76; 3; Indels 0; Gaps 0;

Matches 10; Conservative 2; Mismatches 0; Gaps 0;

Qy 1 RHYGETKMNQSSRS 15

||| ||| ||| ||| |||

Db 232 RTVGATRLNQSSRS 246

RESULT 11

T06733

kinesin homolog F28P10.150 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T06733

R;Quetier, F.; Choisine, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artzi

submitted to the Protein Sequence Database, April 1999

A;Reference number: Z15793

A;Accession: T06733

A;Molecule type: DNA

A;Residues: 1-1070 <QUE>

A;Cross-references: UNIPROT:Q9SV36; EMBL:AL049655; GSPDB:GN00061; ATSP:F28P10.150

A;Experimental source: cultivar Columbia; BAC clone F28P10

C;Genetics:

A;Gene: ATSP:F28P10.150

A;Map position: 3

A;Introns: 113/2; 153/3; 194/3; 256/3; 330/3; 377/1; 427/1; 456/3; 527/3; 572/3; 632/3

C;Superfamily: kinesin-related protein KIP61F; kinesin motor domain homology

F;124-466/Domain: kinesin motor domain homology <KMOT>

Query Match 60.8%; Score 48; DB 2; Length 1070;

Best Local Similarity 66.7%; Pred. No. 1.9; 5; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 RHYGETKMNQSSRS 15

||| ||| ||| ||| |||

Db 311 RHAANTKMNTESSRS 325

RESULT 12

T29898

kinesin protein OSM-3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004

C;Accession: T29898

R;Nelson, J.; Wohlmann, P.

submitted to the EMBL Data Library, September 1996
A;Description: The sequence of C. elegans cosmid M02B7.

A;Reference number: Z20706

A;Accession: T29898

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-670 <NE>

A;Cross-references: EMBL:U70851; PIDN:AAB09128.1; GSPDB:GN00022; CESP:osm-3

A;Experimental source: strain Bristol N2; clone M02B7

C;Genetics:

A;Gene: CESP:osm-3

A;Map position: 4

A;Introns: 18/2; 76/3; 133/3; 197/3; 260/3; 444/1; 478/3; 568/1; 624/1

C;Superfamily: kinesin motor domain homology

Query Match 59.5%; Score 47; DB 2; Length 670;

Best Local Similarity 66.7%; Pred. No. 1.8;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15

||| ||| ||| ||| |||

Db 188 RHVGATLKNKSSRS 202

RESULT 13

S54351

kinesin osm-3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004

C;Accession: S54351

R;Tabish, M.; Siddiqui, Z.K.; Nishikawa, K.; Siddiqui, S.S.

J. Mol. Biol. 247, 377-389, 1995

A;Title: Exclusive expression of C. elegans osm-3 kinesin gene in chemosensory neurons

A;Reference number: S54351; MUID:95230679; PMID:7714894

A;Accession: S54351

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-672 <TAB>

A;Cross-references: UNIPROT:P46873; GB:D38632; NID:G808864; PIDN:BAA07612.1; PID:d100819

C;Superfamily: kinesin motor domain homology

C;Keywords: ATP; nucleotide binding; P-loop

F;48-376/Domain: kinesin motor domain homology <KMOT>

F;130-137/Region: nucleotide-binding motif A (P-loop)

Query Match 59.5%; Score 47; DB 2; Length 672;

Best Local Similarity 66.7%; Pred. No. 1.8;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15

||| ||| ||| ||| |||

Db 235 RHVGATLKNKSSRS 249

RESULT 14

S48020

kinesin-related protein katC - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 14-Jul-1995 #sequence_revision 01-Dec-1995 #text_change 16-Aug-2004

C;Accession: S48020

R;Mitsui, H.; Nakatani, K.; Yamaguchi-Shinozaki, K.; Shinozaki, K.; Takahashi

Plant Mol. Biol. 25, 865-876, 1994

A;Title: Sequencing and characterization of the kinesin-related genes katB and katC of A

A;Reference number: S48019; MUID:94355659; PMID:8075402

A;Accession: S48020

A;Molecule type: mRNA

A;Residues: 1-754 <MIT>

A;Cross-references: UNIPROT:P46875; EMBL:D21138; NID:G1438843; PIDN:BAA04674.1; PID:d100

C;Genetics:

A;Gene: katC

C;Superfamily: kinesin motor domain homology

C;Keywords: ATP; nucleotide binding; P-loop

F;397-739/Domain: kinesin motor domain homology <KMOT>

F;481-488/Region: nucleotide-binding motif A (P-loop)

Query Match 59.5%; Score 47; DB 2; Length 754;

Best Local Similarity 60.0%; Pred. No. 2;

Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15

||| ||| ||| ||| |||

Db 598 RSVGKTQMQEQRSS 612

RESULT 15

S34830

kinesin-related protein katA - Arabidopsis thaliana

N;Alternate names: protein F7J7.210; protein T6K22.10

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 09-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 16-Aug-2004

C;Accession: S34830; T04958; T05170

R;Mitsui, H.; Yamaguchi-Shinozaki, K.; Shinozaki, K.; Takahashi, H.

Mol. Gen. Genet. 238, 362-368, 1993

A;Title: Identification of a gene family (kat) encoding kinesin-like proteins in Arabi

A;Reference number: S34830; MUID:93261419; PMID:8492804

A;Accession: S34830

A;Molecule type: mRNA

A;Residues: 1-793 <MIT>

A;Cross-references: UNIPROT:Q07970; EMBL:D11371; NID:G303501; PIDN:BAA01972.1; PID:d10

R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F

submitted to the Protein Sequence Database, July 1998

A;Reference number: Z15391

A;Accession: T04958

A;Molecule type: DNA

A;Residues: 1-793 <BEV>

A;Cross-references: EMBL:AL021960

A;Experimental source: cultivar Columbia; BAC clone F7J7

R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; M

submitted to the Protein Sequence Database, August 1998

A;Reference number: Z15400

A;Accession: T05170

A;Molecule type: DNA

A;Residues: 1-397 <BEW>

A;Cross-references: EMBL:AL031187

A;Experimental source: cultivar Columbia; BAC clone T6K22

C;Genetics:

A;Gene: katA

A;Map position: 4

A;Introns: 15/3; 89/3; 138/1; 174/3; 214/3; 282/3; 352/3; 377/3; 426/3; 473/1; 509/3;

A;Note: F7J7.210; T6K22.10

C;Superfamily: kinesin motor domain homology

C;Keywords: ATP; nucleotide binding; P-loop

F;432-778/Domain: kinesin motor domain homology <KMOT>

F;516-523/Region: nucleotide-binding motif A (P-loop)

Query Match

59.5%; Score 47; DB 2; Length 793;

Best Local Similarity 60.0%; Pred. No. 2.1;

Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15

||| ||| ||| ||| |||

Db 637 RSVGKTQMQEQRSS 651

Search completed: November 1, 2005, 19:13:42

Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 1, 2005, 18:54:26 ; Search time 171 Seconds
(without alignments)
44.919 Million cell updates/sec

Title: US-09-993-399-1

Perfect score: 79

Sequence: 1 RHYGETMQRSSRS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	2663	1 CENE HUMAN	Q02224 homo sapien
2	71	89.9	160	2 O35059	O35059 mus musculus
3	71	89.9	549	2 O7TPX4	O7TPX4 mus musculus
4	71	89.9	2474	2 O6RT24	O6RT24 mus musculus
5	69	87.3	2954	2 O42263	O42263 xenopus lae
6	58	73.4	807	2 Q94RV9	Q94RV9 arabidopsis
7	58	73.4	823	2 Q9S7F3	Q9S7F3 arabidopsis
8	58	73.4	888	2 Q9LQ62	Q9LQ62 arabidopsis
9	54	68.4	859	2 O6IWZ2	O6IWZ2 leishmania
10	54	68.4	890	2 O6IWZ1	O6IWZ1 leishmania
11	54	68.4	955	1 KINL LEICH	P46865 leishmania
12	53	67.1	2013	2 Q9VKI0	Q9VKI0 drosophila
13	53	67.1	2244	2 Q9NCG0	Q9NCG0 drosophila
14	52	65.8	168	2 O54722	O54722 rattus norv
15	52	65.8	459	2 Q9SS30	Q9SS30 arabidopsis
16	52	65.8	865	2 Q9SL11	Q9SL11 macaca fasc
17	52	65.8	1266	2 Q7PCK6	Q7PCK6 macaca fasc
18	52	65.8	1304	2 Q86VH0	Q86VH0 homo sapien
19	52	65.8	1335	2 Q86VH1	Q86VH1 homo sapien
20	52	65.8	1394	2 Q7MGZ4	Q7MGZ4 mus musculus
21	52	65.8	1394	2 Q7MGZ5	Q7MGZ5 rattus norv
22	52	65.8	1401	2 Q86VH2	Q86VH2 homo sapien
23	52	65.8	1931	2 Q9NCF9	Q9NCF9 drosophila
24	52	65.8	1931	2 Q9VKH9	Q9VKH9 drosophila
25	51	64.6	581	2 Q9SVJ7	Q9SVJ7 arabidopsis
26	51	64.6	834	2 Q9SVJ8	Q9SVJ8 arabidopsis
27	50	63.3	677	2 Q9VRK9	Q9VRK9 drosophila
28	50	63.3	1459	2 P87198	P87198 ustilago ma
29	50	63.3	1624	2 Q9U579	Q9U579 strongyloce
30	49	62.0	146	2 Q91113	Q91113 morone saxa
31	49	62.0	148	2 O35232	O35232 mus musculus

RESULT 1				
CENE HUMAN				
ID	CENE HUMAN	STANDARD;	PRT;	2663 AA.
AC	Q02224;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Centromeric protein E (CENP-E protein).			
GN	Name-CENPE;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93024922; PubMed=1406971; DOI=10.1038/359536a0;			
RA	Yen T.J., Li G., Schaar B.T., Szilak I., Cleveland D.W.;			
RT	"CENP-E is a putative kinetochore motor that accumulates just before			
RT	mitosis.";			
RL	Nature 359:536-539(1992).			
RN	[2]			
RP	CHARACTERIZATION.			
RX	MEDLINE=95196755; PubMed=7889940;			
RA	Thrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.;			
RT	"Mitotic HeLa cells contain a CENP-E-associated minus end-directed			
RT	microtubule motor.";			
RL	EMBO J. 14:918-926(1995).			
RN	[3]			
RP	CHARACTERIZATION.			
RX	MEDLINE=98437347; PubMed=9763420; DOI=10.1083/jcb.143.1.49;			
RA	Chan G.K.T., Schaar B.T., Yen T.J.;			
RT	"Characterization of the kinetochore binding domain of CENP-E reveals			
RT	interactions with the kinetochore proteins CENP-F and hBUBR1.";			
RL	J. Cell Biol. 143:49-63(1998).			
RN	[4]			
RP	FARNESYLATION.			
RX	MEDLINE=20459117; PubMed=10852915; DOI=10.1074/jbc.M00346200;			
RA	Asar H.R., James L., Gray K., Carr D., Black S., Armstrong L.,			
RA	Bishop W.R., Kirschmeier P.;			
RT	"Farnesyl transferase inhibitors block the farnesylation of CENP-E and			
RT	CENP-F and alter the association of CENP-E with the microtubules.";			
RL	J. Biol. Chem. 275:30451-30457(2000).			
CC	-!- FUNCTION: Minus-end directed microtubule motor. Probable			
CC	kinetochore motor. Accumulates just before mitosis at the G2 phase			
CC	of the cell cycle. Probably important for chromosome movement			
CC	and/or spindle elongation.			
CC	-!- SUBUNIT: Interacts with CENP-F and BUBR1 kinase.			
CC	-!- SUBCELLULAR LOCATION: Associates with kinetochores during			
CC	congression, relocates to the spindle midzone at anaphase, and is			
CC	quantitatively discarded at the end of the cell division.			
CC	-!- SIMILARITY: Belongs to the kinesin-like protein family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			

O15719 dictyosteli
O84j18 arabidopsis
O9mau7 arabidopsis
Q991c7 mus musculu
Q14807 homo sapien
O869b8 dictyosteli
Q9avd7 nicotiana t
Q651z7 oryza sativ
O7yyj8 cryptospori
Q9svj6 arabidopsis
Q9ul42 leishmania
Q9ul79 leishmania
Q9neb6 leishmania
Q93xf8 zea mays (m

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CC EMBL; Z15005; CAA78727.1; -.
CC PIR; S28261; S28261.
CC HSP; P17119; 1F9T.
CC MIM; 117143; -.
CC Genew; HGNC:1856; CENPE.
CC GO; GO:0000776; C:kinetochore; TAS.
CC GO; GO:0005634; C:nucleus; TAS.
CC GO; GO:0003777; F:DNA replication and chromosome cycle; TAS.
CC GO; GO:0000067; P:DNA replication and chromosome cycle; TAS.
CC GO; GO:0007079; P:mitotic chromosome movement; TAS.
CC GO; GO:0007080; P:mitotic metaphase plate congression; TAS.
CC InterPro; IPR001752; Kinesin_motor.
CC Pfam; PF00225; Kinesin; 1.
CC PRINTS; PR00380; KINESINHEAVY.
CC SMART; SM00129; KISC; 1.
CC PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
CC PROSITE; PS00067; KINESIN MOTOR DOMAIN2; 1.
CC ATP-binding; Cell cycle; Cell division; Centromere; Coiled coil;
KW Lipoprotein; Microtubule; Mitosis; Motor protein; Prenylation.
FT DOMAIN 1 335
FT BINDING 336 2471 Coiled coil (Potential).
FT BINDING 2472 2663 Globular (Potential).
FT BINDING 86 93 ATP (By similarity).
FT LIPID 2660 2660 S-farnesyl cysteine.
SQ SEQUENCE 2663 AA; 312087 MW; CFCF13880C8C8CB8 CRC64;
Query Match 100.0%; Score 79; DB 1; Length 2663;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSSRS 15
DB 189 RHYGETKNQSRSSRS 203

RESULT 2
ID O35059 PRELIMINARY; PRT; 160 AA.
AC O35059;
DT 01-JAN-1998 (TrEMBLrel. 05 Created)
DT 01-JAN-1998 (TrEMBLrel. 05; Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26; Last annotation update)
DE Motor domain of Kif10 (Fragment).
GN Name=Cenpe;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Egg;
MEDLINE=97420736; PubMed=9275178; DOI=10.1073/pnas.94.18.9654;
RA Nakagawa T., Tanaka Y., Matsuo E., Kondo S., Okada Y., Noda Y.,
RA Kanai Y., Hirokawa N.;
RT "Identification and classification of 16 new kinesin superfamily (KIF)
RT proteins in mouse genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9654-9659(1997).
DR EMBL; AB001426; BAA22386.1; -.
DR EMBL; AB001426; BAA22386.1; -.
DR HSP; P17119; 1F9V.
DR MGD; MGI:1098230; Cenpe.
DR GO; GO:0008608; P:spindle kinetochore attachment; TAS.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00067; KINESIN MOTOR DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein.

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FT NON_TER 1 1
FT NON_TER 160 160
SQ SEQUENCE 160 AA; 18406 MW; 9E6E4F6E2642C241 CRC64;
Query Match 89.9%; Score 71; DB 2; Length 160;
Best Local Similarity 93.3%; Pred. No. 4.9e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSSRS 15
DB 108 RHYGETKNQSRSSRS 122

RESULT 3
ID Q7TPX4 PRELIMINARY; PRT; 549 AA.
AC Q7TPX4;
DT 01-OCT-2003 (TrEMBLrel. 25; Created)
DT 01-OCT-2003 (TrEMBLrel. 25; Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26; Last annotation update)
DE Cenpe protein (Fragment).
GN Name=Cenpe;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Egg;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Egg;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052843; AAH52843.1; -.
DR HSP; P17119; 1F9T.
DR GO; GO:0008608; P:spindle kinetochore attachment; TAS.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS00067; KINESIN MOTOR DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein.
FT NON_TER 549 549
SQ SEQUENCE 549 AA; 62899 MW; B707C97DC9FB38D3 CRC64;
Query Match 89.9%; Score 71; DB 2; Length 549;
Best Local Similarity 93.3%; Pred. No. 0.0003;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSSRS 15
DB 108 RHYGETKNQSRSSRS 122

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Db      189 RHYGITKNQSRSS 203

RESULT 4
Q6RT24
ID      O6RT24      PRELIMINARY;      PRT; 2474 AA.
AC
DT      05-JUL-2004 (TREMBLrel. 27, Created)
DT      05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE      Centromere associated protein-E.
GN      Name=Centpe;
OS      Mus musculus (Mouse)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22806743; PubMed=12925705; DOI=10.1083/jcb.200303167;
RA      Weaver B.A., Bonday Z.Q., Putkey F.R., Kops G.J., Silk A.D.,
RA      Cleveland D.W.;
RT      "Centromere-associated protein-E is essential for the mammalian
RT      mitotic checkpoint to prevent aneuploidy due to single chromosome
RT      loss.";
RL      J. Cell Biol. 162:551-563 (2003).
DR      EMBL; AY493378; AAR5499.1; -.
DR      GO; GO:0008608; P:spindle kinetochore attachment; TAS.
DR      InterPro; IPR001752; Kinesin_motor.
DR      Pfam; PF00225; Kinesin; 1.
DR      PRINTS; PR00380; KINESINHEAVY.
DR      SMART; SM00129; KISC; 1.
DR      PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR      PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
DR      PROSITE; PS00213; LIPOCALIN; UNKNOWN 1.
KW      ATP-binding; Microtubule; Motor protein.
SQ      SEQUENCE 2474 AA; 286523 MW; BAF52DD6068A2903 CRC64;

Query Match      89.9%; Score 71; DB 2; Length 2474;
Best Local Similarity 93.3%; Pred. No. 0.0012;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RHYGITKNQSRSS 15
      ||||| ||||| |||||
Db      189 RHYGITKNQSRSS 203

RESULT 5
O42263
ID      O42263      PRELIMINARY;      PRT; 2954 AA.
AC
DT      01-JAN-1998 (TREMBLrel. 05, Created)
DT      01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT      01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE      Kinesin-related protein.
GN      Name=XCEP-E;
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98028574; PubMed=9363944; DOI=10.1016/S0092-8674(00)80419-5;
RA      Wood K.W., Sakowicz R., Goldstein L.S., Cleveland D.W.;
RT      "CENP-E is a plus end-directed kinetochore motor required for
RT      metaphase chromosome alignment.";
RL      Cell 91:357-366 (1997).
DR      EMBL; AF027728; AAC60300.1; -.
DR      PIR; T14156; T14156.
DR      HSSP; P17119; 1F9T.
DR      GO; GO:0005875; C:microtubule associated complex; IEA.
DR      GO; GO:0005524; F:ATP binding; IEA.

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DR      GO; GO:0003774; F:motor activity; IEA.
DR      InterPro; IPR001752; Kinesin_motor.
DR      Pfam; PF00225; Kinesin; 1.
DR      PRINTS; PR00380; KINESINHEAVY.
DR      SMART; SM00129; KISC; 1.
DR      PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR      PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
KW      ATP-binding; Microtubule; Motor protein.
SQ      SEQUENCE 2954 AA; 339966 MW; 439804ED0592679 CRC64;

Query Match      87.3%; Score 69; DB 2; Length 2954;
Best Local Similarity 86.7%; Pred. No. 0.0033;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 RHYGETKNQSRSS 15
      ||||| ||||| |||||
Db      187 RHYGETKNQSRSS 201

RESULT 6
Q94HV9
ID      Q94HV9      PRELIMINARY;      PRT; 807 AA.
AC
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE      Kinesin motor protein (Kin2), putative.
GN      Name=T4M14.11;
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC      eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Town C.D., Haas B.J., Wu D., Maiti R., Hannick L.I., Chan A.P.,
RA      Tallon L.J., Rooney T., Utterback T.R., VanAken S.E., Feldblum T.V.,
RA      White O., Fraser C.M.;
RL      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Lin X., Kaul S.;
RL      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Town C.D., Kaul S.;
RL      Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AC027036; AAK62792.1; -.
DR      HSSP; P20480; IN6M.
DR      GO; GO:0005875; C:microtubule associated complex; IEA.
DR      GO; GO:0005524; F:ATP binding; IEA.
DR      GO; GO:0003774; F:motor activity; IEA.
DR      InterPro; IPR001752; Kinesin_motor.
DR      Pfam; PF00225; Kinesin; 1.
DR      PRINTS; PR00380; KINESINHEAVY.
DR      SMART; SM00129; KISC; 1.
DR      PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR      PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
KW      ATP-binding; Microtubule; Motor protein.
SQ      SEQUENCE 807 AA; 91260 MW; FD7CDAD68EA30C28 CRC64;

Query Match      73.4%; Score 58; DB 2; Length 807;
Best Local Similarity 73.3%; Pred. No. 0.086;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 RHYGETKNQSRSS 15
      ||||| ||||| |||||
Db      184 RHYGETKNQSRSS 198

RESULT 7
Q9S7P3
ID      Q9S7P3      PRELIMINARY;      PRT; 823 AA.

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AC Q957P3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Kinesin-like protein.
 GN Name=ZCF125;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ooe H., Kato A., Komeda Y.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20018182; PubMed=10548732; DOI=10.1016/S0378-1119(99)00403-5;
 RA Kato A., Suzuki M., Kuwahara A., Ooe H., Higano-Inaba K., Komeda Y.;
 RT "Isolation and analysis of cDNA within a 300 kb Arabidopsis thaliana
 RT genomic region located around the 100 map unit of chromosome 1.";
 RL Gene 239:309-316(1999).
 DR EMBL; AB028470; BAA88114.1; -;
 DR EMBL; AB028468; BAA88112.1; -;
 DR PIR; T52425; T52425.
 DR HSSP; P20480; INGM.
 DR GO; GO:0005875; C:microtubule associated complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
 DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein.
 SQ SEQUENCE 823 AA; 93148 MW; 6AFB1C622E4632C9 CRC64;
 Query Match 73.4%; Score 58; DB 2; Length 823;
 Best Local Similarity 73.3%; Pred. No. 0.088;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RHYGETKNQSRSSRS 15
 DB 184 RHFGETNNVHSSRS 198
 ID Q9LQ62 PRELIMINARY; PRT; 888 AA.
 AC Q9LQ62;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE T30E16.9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chao Q., Brooks S., Buehler E., Dunn P., Khan S., Kim C., Shinn P.,
 RA Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.P.,
 RA Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S., Lueros S.,
 RA Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis R.W.,
 RA Federspiel N.A., Theologis A., Ecker J.R.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bai B., Chin C., Chiou J., Choi E.,
 RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,

RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Theologis A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC009317; AAF79747.1; -;
 DR PIR; D96619; D96619.
 DR HSSP; P20480; INGM.
 DR GO; GO:0005875; C:microtubule associated complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
 DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein.
 SQ SEQUENCE 888 AA; 100694 MW; 0D640FBACEE01B5 CRC64;
 Query Match 73.4%; Score 58; DB 2; Length 888;
 Best Local Similarity 73.3%; Pred. No. 0.096;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RHYGETKNQSRSSRS 15
 DB 215 RHFGETNNVHSSRS 229
 ID Q6IW22 PRELIMINARY; PRT; 859 AA.
 AC Q6IW22;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Kinesin related protein (fragment).
 OS Leishmania donovani.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5661;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KE16;
 RA Sivakumar R., Singh S.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY615886; AAT40474.1; -;
 DR GO; GO:0005875; C:microtubule associated complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein.
 FT NON TER 859 859
 SQ SEQUENCE 859 AA; 95590 MW; 7F941034DACA2155 CRC64;
 Query Match 68.4%; Score 54; DB 2; Length 859;
 Best Local Similarity 73.3%; Pred. No. 0.52;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RHYGETKNQSRSSRS 15
 DB 241 RHTASTKMDRSSRS 255
 ID Q6IW21 PRELIMINARY; PRT; 890 AA.
 AC Q6IW21;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)


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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Kinesin related protein (Fragment).
OS Leishmania donovani.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5661;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DD8;
RA Sivakumar R., Singh S.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY615887; AAT40475.1; -.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR InterPro; IPR001752; Kinesin_motor.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
DR SUBSITE; SUBSITE138; SUBTILASE_SER; UNKNOWN 1.
KW ATP-binding; Microtubule; Motor protein.
FT NON TER 890
SQ SEQUENCE 890 AA; 98732 MW; 1AFF4AFD0F905407 CRC64;

Query Match 68.4%; Score 54; DB 2; Length 890;
Best Local Similarity 73.3%; Pred. No. 0.54;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKMQRSRS 15
Db 240 RHTASTKMDRSRS 254

RESULT 11
KINL_LEICH STANDARD; PRT; 955 AA.
AC P46865;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Kinesin-like protein K39 (Fragment).
GN Name=KIN;
OS Leishmania chagasi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=44271;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MHOM/BR/92/BA-2;
RX MEDLINE=93133867; PubMed=8421715;
RA Burns J.M. Jr., Shreffler W.G., Benson D.R., Ghalib H.W., Badaro R.,
RA Reed S.G.;
RT "Molecular characterization of a kinesin-related antigen of Leishmania
RT chagasi that detects specific antibody in African and American
RT visceral leishmaniasis."
RT Proc. Natl. Acad. Sci. U.S.A. 90:775-779(1993).
CC -|- DEVELOPMENTAL STAGE: Predominant in amastigotes.
CC -|- SIMILARITY: Belongs to the kinesin-like protein family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L07879; AAA29254.1; -.
DR PIR; A47334; A47334.
DR HSSP; P17119; 3KAR.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.

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DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Coiled coil; Microtubule; Motor protein; Repeat.
FT DOMAIN 1 399
FT DOMAIN 426 >955
FT NP_BIND 122 129
FT DOMAIN 704 >955
FT REPEAT 704 742
FT REPEAT 743 781
FT REPEAT 782 820
FT REPEAT 821 859
FT REPEAT 860 898
FT REPEAT 899 937
FT REPEAT 938 >955
FT NON TER 955
SQ SEQUENCE 955 AA; 106168 MW; 8CA76815B8B4C6E9 CRC64;

Query Match 68.4%; Score 54; DB 1; Length 955;
Best Local Similarity 73.3%; Pred. No. 0.58;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKMQRSRS 15
Db 241 RHTASTKMDRSRS 255

RESULT 12
Q9VK10 PRELIMINARY; PRT; 2013 AA.
AC Q9VK10;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG6392-PA.
GN Name=cmet; ORFNames=CG6392;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borchan M.R., Bouck J., Brockstein P., Brotier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

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Search completed: November 1, 2005, 19:13:03
Job time : 178 secs

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RL Mol. Biol. Cell 7:289-305(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Testes;
RA Sperry A.O.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF035954; AAB88702.1; -.
DR HSSP; P17119; 1F9V.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00225; Kinesin; 1.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00067; KINESIN_MOTOR_DOMAIN2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
KW ATP-binding; Microtubule; Motor protein.
FT NON_TER 1
FT NON_TER 168 168
SQ SEQUENCE 168 AA; 18751 MW; D961E4CD1BDAAB7 CRC64;
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Query Match 65.8%; Score 52; DB 2; Length 168;
Best Local Similarity 66.7%; Pred. No. 0.19;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 RHVGETKNQKRSRS 15
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Db 114 RHGTQTQNNHSSRS 128
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RESULT 15
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AC Q9SS30;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative kinesin-like centromere protein.
GN Name=F14P13.22;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC009400; AAF02823.1; -.
DR HSSP; P17119; 1F9T.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein.
SQ SEQUENCE 459 AA; 51872 MW; 7C8487E9B7038E6A CRC64;
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Query Match 65.8%; Score 52; DB 2; Length 459;
Best Local Similarity 73.3%; Pred. No. 0.59;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 RHVGETKNQKRSRS 15
||| ||| ||| |||
Db 182 RHGTQTQNNHSSRS 196
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 1, 2005, 18:44:05 ; Search time 41 Seconds
(without alignments)
27.311 Million cell updates/sec

Title: US-09-993-399-1

Perfect score: 79

Sequence: 1 RHYGETKNQSRSSRS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*

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5: /cgn2_6/ptodata/1/iaa/6C COMB.pcp.*

6: /cgn2_6/ptodata/1/iaa/6D COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	2662	4	US-09-595-684B-31
2	79	100.0	2662	4	US-09-538-092-1252
3	69	87.3	2954	4	US-09-150-867-1
4	54	68.4	955	1	US-08-006-676B-1
5	54	68.4	955	1	US-08-282-845-2
6	54	68.4	955	2	US-08-428-414A-3
7	54	68.4	955	5	PCT-US94-00324-1
8	52	65.8	341	3	US-09-724-517-4
9	52	65.8	341	4	US-09-641-807A-4
10	52	65.8	341	4	US-09-723-096-4
11	52	65.8	1279	3	US-09-724-517-2
12	52	65.8	1279	4	US-09-641-807A-2
13	52	65.8	1279	4	US-09-723-096-2
14	49	62.0	346	3	US-09-724-224-6
15	49	62.0	346	4	US-10-093-317-6
16	49	62.0	370	3	US-09-724-224-2
17	49	62.0	370	4	US-10-093-317-2
18	49	62.0	487	3	US-09-724-224-8
19	49	62.0	487	4	US-10-093-317-8
20	49	62.0	490	4	US-09-949-016-8784
21	49	62.0	512	3	US-09-724-224-4
22	49	62.0	512	4	US-10-093-317-4
23	49	62.0	665	4	US-09-595-684B-35
24	48	60.8	324	3	US-09-183-861-53
25	48	60.8	324	3	US-09-022-765-53
26	48	60.8	324	4	US-09-551-974A-53
27	48	60.8	324	4	US-09-565-501A-53

28 60.8 324 4 US-09-639-206A-53
29 48 60.8 324 4 US-09-874-923-53
30 45 57.0 411 2 US-08-713-815A-4
31 45 57.0 441 2 US-08-713-815A-3
32 45 57.0 915 4 US-09-949-016-7425
33 45 57.0 956 4 US-09-914-259-17
34 45 57.0 957 4 US-09-914-259-16
35 45 57.0 963 4 US-09-914-259-20
36 45 57.0 963 4 US-09-914-259-22
37 45 57.0 963 4 US-09-538-092-1060
38 45 57.0 967 4 US-09-914-259-21
39 45 57.0 975 4 US-09-914-259-19
40 45 57.0 978 4 US-09-949-016-10196
41 45 57.0 1027 4 US-09-914-259-27
42 45 57.0 1031 4 US-09-914-259-24
43 45 57.0 1032 4 US-09-914-259-26
44 45 57.0 1032 4 US-09-538-092-1293
45 44 55.7 683 4 US-09-252-991A-26189

ALIGNMENTS

RESULT 1

US-09-595-684B-31
; Sequence 31, Application US/09595684B
; Patent No. 6544766
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Ohashi, Cara
; APPLICANT: Sakowicz, Roman
; APPLICANT: Vaisberg, Eugeni
; APPLICANT: Wood, Kenneth
; APPLICANT: Yu, Ming
; TITLE OF INVENTION: Human kinesins and methods of producing
; FILE REFERENCE: cytop036
; CURRENT APPLICATION NUMBER: US/09595,684B
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/295,612
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; TYPE: PRT
; LENGTH: 2662
; ORGANISM: Human
US-09-595-684B-31

Query Match 100.0%; Score 79; DB 4; Length 2662;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSSRS 15

Db 189 RHYGETKNQSRSSRS 203

RESULT 2

US-09-538-092-1252
; Sequence 1252, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01

; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratPatSeqFormatter Version 0.9
; SEQ ID NO 1252
; LENGTH: 2663
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q02224
US-09-538-092-1252

Query Match 100.0%; Score 79; DB 4; Length 2663;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
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Db 189 RHYGETKNQRRSSRS 203

RESULT 3

US-09-150-867-1
; Sequence 1, Application US/09150867
; Patent No. 6645748
; GENERAL INFORMATION:
; APPLICANT: Wood, Kenneth W.
; APPLICANT: Sakowicz, Roman
; APPLICANT: Goldstein, Lawrence S.B.
; APPLICANT: Cleveland, Don W.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Plus End-Directed Microtubule Motor Required for
; FILE OF INVENTION: Chromosome Congression
; FILE REFERENCE: 18557C-000110US
; CURRENT APPLICATION NUMBER: US/09/150,867
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: US 60/058,645
; EARLIER FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2954
; TYPE: PRT
; ORGANISM: Xenopus sp.
; FEATURE:
; OTHER INFORMATION: Xenopus centromere-associated protein-E (XCENP-E)
; OTHER INFORMATION: member of the kinesin superfamily of microtubule
; OTHER INFORMATION: motor proteins
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(472)
; OTHER INFORMATION: kinesin like motor domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (473)..(2752)
; OTHER INFORMATION: rod domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (2753)..(2954)
; OTHER INFORMATION: tail domain
US-09-150-867-1

Query Match 87.3%; Score 69; DB 4; Length 2954;
Best Local Similarity 86.7%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
|||||
Db 187 RHYGETKNQRRSSRS 201

RESULT 4

US-08-006-676B-1

; Sequence 1, Application US/08006676B
; Patent No. 5411865
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven
; TITLE OF INVENTION: Diagnosis of Leishmaniasis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jeffrey B. Oster
; STREET: 8339 SE 57th Street
; CITY: Mercer Island
; STATE: Washington
; COUNTRY: USA
; ZIP: 98040-4906
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/006,676B
; FILING DATE: 15-JAN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oster, Jeffrey B.
; REGISTRATION NUMBER: 32,585
; REFERENCE/DOCKET NUMBER: REED-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 232 7845
; TELEFAX: (206) 236 0205
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 955 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-006-676B-1
Query Match 68.4%; Score 54; DB 1; Length 955;
Best Local Similarity 73.3%; Pred. No. 0.22;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 RHYGETKNQRRSSRS 15
|||||
Db 241 RHTASTKNQRRSSRS 255
RESULT 5
US-08-282-845-2
; Sequence 2, Application US/08282845
; Patent No. 5719263
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: A 230kd Antigen Present in Leishmania
; TITLE OF INVENTION: Species
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Macintosh Operating System 7.1
; SOFTWARE: Microsoft Word for Macintosh 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,845
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/006,676

1 FILING DATE: JANUARY 15, 1993
2 CLASSIFICATION: 435
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Perkins, Patricia Anne
5 REGISTRATION NUMBER: 34,693
6 REFERENCE/DOCKET NUMBER: 5004-A
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: (206)587-0430
9 TELEFAX: (206)233-0644
10 INFORMATION FOR SEQ ID NO: 2:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 955 amino acids
13 TYPE: amino acid
14 TOPOLOGY: linear
15 MOLECULE TYPE: protein
16 US-08-282-845-2

Query Match 68.4%; Score 54; DB 1; Length 955;
Best Local Similarity 73.3%; Pred. No. 0.22;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNORSSRS 15
Db 241 RHTASTKNDRSSRS 255

1 RESULT 6
2 US-08-428-414A-3
3 Sequence 3, Application US/08428414A
4 Patent No. 5912166
5 GENERAL INFORMATION:
6 APPLICANT: Reed, Steven G.
7 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
8 LEISHMANIASIS
9 NUMBER OF SEQUENCES: 5
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: SEED AND BERRY
12 STREET: 6300 Columbia Center, 701 Fifth Avenue
13 CITY: Seattle
14 STATE: Washington
15 COUNTRY: USA
16 ZIP: 98104-7092
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 OPERATING SYSTEM: IBM PC compatible
20 SOFTWARE: PatentIn Release #1.0, Version #1.30
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/428,414A
23 FILING DATE: 21-APR-1995
24 CLASSIFICATION: 436
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Kadlecsek, Ann T.
27 REGISTRATION NUMBER: 39,244
28 REFERENCE/DOCKET NUMBER: 210121.407
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (206) 622-4900
31 TELEFAX: (206) 682-6031
32 TELEX: 3723836 SEEDANDBERRY
33 INFORMATION FOR SEQ ID NO: 3:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 955 amino acids
36 TYPE: amino acid
37 STRANDEDNESS:
38 TOPOLOGY: linear
39 US-08-428-414A-3

Query Match 68.4%; Score 54; DB 2; Length 955;
Best Local Similarity 73.3%; Pred. No. 0.22;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNORSSRS 15
Db 241 RHTASTKNDRSSRS 255

1 Db 241 RHTASTKNDRSSRS 255
2 PCT-US94-00324-1
3 Sequence 1, Application PC/TUS9400324
4 GENERAL INFORMATION:
5 APPLICANT: Reed, Steven
6 TITLE OF INVENTION: Diagnosis of Leishmaniasis
7 NUMBER OF SEQUENCES: 3
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Immunex Corporation
10 STREET: 51 University Street
11 CITY: Seattle
12 STATE: Washington
13 COUNTRY: USA
14 ZIP: 98101
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: Apple Macintosh
18 OPERATING SYSTEM: Apple System 7.1
19 SOFTWARE: Microsoft Word, version 5.1a
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: PCT/US94/00324
22 FILING DATE:
23 CLASSIFICATION:
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US/08/006,676
26 FILING DATE: 15-JAN-1993
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Perkins, Patricia Anne
29 REGISTRATION NUMBER: 34,693
30 REFERENCE/DOCKET NUMBER: 5004-WO
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (206) 587-0430
33 TELEFAX: (206) 233-0644
34 INFORMATION FOR SEQ ID NO: 1:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 955 amino acids
37 TYPE: amino acid
38 TOPOLOGY: linear
39 MOLECULE TYPE: protein
40 PCT-US94-00324-1

Query Match 68.4%; Score 54; DB 5; Length 955;
Best Local Similarity 73.3%; Pred. No. 0.22;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNORSSRS 15
Db 241 RHTASTKNDRSSRS 255

1 RESULT 8
2 US-09-724-517-4
3 Sequence 4, Application US/09724517
4 Patent No. 6379941
5 GENERAL INFORMATION:
6 APPLICANT: Beraud, Christophe
7 APPLICANT: Freedman, Richard
8 TITLE OF INVENTION: No. 6379941el motor proteins and methods for
9 their use
10 FILE REFERENCE: 1031
11 CURRENT APPLICATION NUMBER: US/09/724,517
12 CURRENT FILING DATE: 2000-11-27
13 PRIOR APPLICATION NUMBER: US/09/641,807
14 PRIOR FILING DATE: 2000-08-17
15 NUMBER OF SEQ ID NOS: 4
16 SOFTWARE: FastSeq for Windows Version 4.0
17 SEQ ID NO 4
18 LENGTH: 341
19 TYPE: PRT
20 ORGANISM: Human

US-09-724-517-4

Query Match 65.8%; Score 52; DB 3; Length 341;
Best Local Similarity 66.7%; Pred. No. 0.17;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RHYGETKNQRRSSRS 15
DB 192 RHTGTTQNNHSSRS 206

RESULT 9

US-09-641-807A-4
; Sequence 4, Application US/09641807A
; Patent No. 6440731
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6440731lel motor proteins and methods for
; FILE REFERENCE: 1031
; CURRENT APPLICATION NUMBER: US/09/641,807A
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Human
US-09-641-807A-4

Query Match 65.8%; Score 52; DB 4; Length 341;
Best Local Similarity 66.7%; Pred. No. 0.17;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
DB 192 RHTGTTQNNHSSRS 206

RESULT 10

US-09-723-096-4
; Sequence 4, Application US/09723096
; Patent No. 6448026
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6448026lel motor proteins and methods for
; FILE REFERENCE: 1031
; CURRENT APPLICATION NUMBER: US/09/723,096
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US/09/641,807
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Human
US-09-723-096-4

Query Match 65.8%; Score 52; DB 4; Length 341;
Best Local Similarity 66.7%; Pred. No. 0.17;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
DB 192 RHTGTTQNNHSSRS 206

RESULT 11

US-09-724-517-2

; Sequence 2, Application US/09724517
; Patent No. 6379941
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6379941lel motor proteins and methods for
; FILE REFERENCE: 1031
; CURRENT APPLICATION NUMBER: US/09/724,517
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US/09/641,807
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1279
; TYPE: PRT
; ORGANISM: Human
; NAME/KEY: VARIANT
; LOCATION: (409)...(436)
; OTHER INFORMATION: Xaa = any amino acid
US-09-724-517-2

Query Match 65.8%; Score 52; DB 3; Length 1279;
Best Local Similarity 66.7%; Pred. No. 0.7;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
DB 194 RHTGTTQNNHSSRS 208

RESULT 12

US-09-641-807A-2
; Sequence 2, Application US/09641807A
; Patent No. 6440731
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6440731lel motor proteins and methods for
; FILE REFERENCE: 1031
; CURRENT APPLICATION NUMBER: US/09/641,807A
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1279
; TYPE: PRT
; ORGANISM: Human
; NAME/KEY: VARIANT
; LOCATION: (409)...(446)
; OTHER INFORMATION: Xaa = any amino acid
US-09-641-807A-2

Query Match 65.8%; Score 52; DB 4; Length 1279;
Best Local Similarity 66.7%; Pred. No. 0.7;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
DB 194 RHTGTTQNNHSSRS 208

RESULT 13

US-09-723-096-2
; Sequence 2, Application US/09723096
; Patent No. 6448026
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard

; TITLE OF INVENTION: No. 6448026el motor proteins and methods for
; FILE OF INVENTION: their use
; FILE REFERENCE: 1031
; CURRENT APPLICATION NUMBER: US/09/723,096
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US/09/641,807
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1279
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (409)...(436)
; OTHER INFORMATION: Xaa = any amino acid
US-09-723-096-2

Query Match 65.8%; Score 52; DB 4; Length 1279;
Best Local Similarity 66.7%; Pred. No. 0.7;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
DB 194 RHTGTTQNEHSSRS 208

RESULT 14
US-09-724-224-6
; Sequence 6, Application US/09724224
; Patent No. 6387644
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6387644el motor proteins and methods for
; FILE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/09/724,224
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Human
US-09-724-224-6

Query Match 62.0%; Score 49; DB 3; Length 346;
Best Local Similarity 66.7%; Pred. No. 0.61;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
DB 208 RTVGATRLNQSSRS 222

RESULT 15
US-10-093-317-6
; Sequence 6, Application US/10093317
; Patent No. 6762043
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6762043el motor proteins and methods for
; FILE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/093,317
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/724,224
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Human
US-10-093-317-6

Query Match 62.0%; Score 49; DB 4; Length 346;
Best Local Similarity 66.7%; Pred. No. 0.61;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
DB 208 RTVGATRLNQSSRS 222

Search completed: November 1, 2005, 18:54:21
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: November 1, 2005, 18:50:35 ; Search time 166 seconds
(without alignments)
37.775 Million cell updates/sec

Title: US-09-993-399-1

Perfect score: 79

Sequence: 1 RHYGETKMNQSSRS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 1865214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	79	100.0	355	18 US-10-517-510-4	Sequence 4, Appli
2	79	100.0	496	18 US-10-517-510-2	Sequence 2, Appli
3	79	100.0	2503	17 US-10-828-985A-11	Sequence 11, Appl
4	79	100.0	2543	17 US-10-828-985A-9	Sequence 9, Appli
5	79	100.0	2568	17 US-10-828-985A-7	Sequence 7, Appli
6	79	100.0	2633	18 US-10-450-763-36864	Sequence 36864, A
7	79	100.0	2663	16 US-10-723-860-749	Sequence 749, App
8	69	87.3	2954	18 US-10-650-280-1	Sequence 1, Appli
9	65	82.3	668	16 US-10-425-115-263022	Sequence 263022,
10	65	82.3	694	15 US-10-425-114-59725	Sequence 59725, A
11	63	79.7	201	16 US-10-437-963-116808	Sequence 116808,

12	53	67.1	2013	20	US-11-097-143-13758	Sequence 13758, A
13	52	65.8	154	11	US-09-864-408A-1218	Sequence 1218, Ap
14	52	65.8	1382	16	US-10-437-963-176714	Sequence 176714,
15	52	65.8	1401	15	US-10-287-226-142	Sequence 142, App
16	52	65.8	1931	20	US-11-097-143-9828	Sequence 9828, Ap
17	51	64.6	197	16	US-10-425-115-245875	Sequence 245875,
18	50	63.3	677	20	US-11-097-143-22341	Sequence 22341, A
19	49	62.0	259	16	US-10-425-115-210540	Sequence 210540,
20	49	62.0	346	16	US-10-797-893-6	Sequence 6, Appli
21	49	62.0	370	16	US-10-797-893-2	Sequence 2, Appli
22	49	62.0	460	9	US-09-925-300-1228	Sequence 1228, Ap
23	49	62.0	487	16	US-10-797-893-8	Sequence 8, Appli
24	49	62.0	490	15	US-10-334-143-80	Sequence 80, Appl
25	49	62.0	512	16	US-10-797-893-4	Sequence 4, Appli
26	49	62.0	665	16	US-10-733-878-425	Sequence 425, App
27	48	60.8	324	9	US-09-874-923-53	Sequence 53, Appli
28	48	60.8	324	9	US-09-991-496-53	Sequence 53, Appli
29	48	60.8	420	16	US-10-437-963-114373	Sequence 114373,
30	48	60.8	821	16	US-10-437-963-114370	Sequence 114370,
31	48	60.8	906	16	US-10-437-963-163527	Sequence 163527,
32	47	59.5	54	10	US-09-826-734-144	Sequence 144, App
33	47	59.5	75	15	US-10-424-599-152360	Sequence 152360,
34	47	59.5	78	16	US-10-425-115-201216	Sequence 201216,
35	47	59.5	247	15	US-10-424-599-156142	Sequence 156142,
36	47	59.5	272	15	US-10-424-599-274019	Sequence 274019,
37	47	59.5	458	15	US-10-369-493-5967	Sequence 5967, Ap
38	47	59.5	670	15	US-10-425-114-59085	Sequence 59085, A
39	47	59.5	789	16	US-10-425-115-200354	Sequence 200354,
40	46	58.2	782	16	US-10-437-963-173873	Sequence 173873,
41	46	58.2	788	16	US-10-437-963-173884	Sequence 173884,
42	46	58.2	932	16	US-10-473-276-1	Sequence 1, Appli
43	45	57.0	114	16	US-10-437-963-113879	Sequence 113879,
44	45	57.0	252	16	US-10-767-701-36255	Sequence 36255, A
45	45	57.0	312	15	US-10-424-599-174384	Sequence 174384,

ALIGNMENTS

RESULT 1

US-10-517-510-4

Sequence 4, Application US/10517510

Publication No. US20050164201A1

GENERAL INFORMATION:

APPLICANT: Harvey, Diane Marie

APPLICANT: Yang, Yi

APPLICANT: Kohl, Nancy

TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE ENCODING

TITLE OF INVENTION: A NOVEL CENTROMERE-ASSOCIATED MOTOR PROTEIN, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 21023P

CURRENT APPLICATION NUMBER: US/10/517,510

CURRENT FILING DATE: 2004-12-10

PRIOR APPLICATION NUMBER: PCT/US03/18203

PRIOR FILING DATE: 2003-06-09

PRIOR APPLICATION NUMBER: 60/387,403

PRIOR FILING DATE: 2002-06-10

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 355

TYPE: PRT

ORGANISM: Human

US-10-517-510-4

Query Match 100.0%; Score 79; DB 18; Length 355;

Best Local Similarity 100.0%; Pred. No. 1.4e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15

DB 189 RHYGETKMNQSSRS 203

RESULT 2
US-10-517-510-2
; Sequence 2, Application US/10517510
; Publication No. US20050164201A1
; GENERAL INFORMATION:
; APPLICANT: Harvey, Diane Marie
; APPLICANT: Yang, Yi
; APPLICANT: Kohl, Nancy
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE ENCODING
; TITLE OF INVENTION: A NOVEL CENTROMERE-ASSOCIATED MOTOR PROTEIN, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 21023P
; CURRENT APPLICATION NUMBER: US/10/517,510
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: PCT/US03/18203
; PRIOR FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: 60/387,403
; PRIOR FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Human
US-10-517-510-2

Query Match 100.0%; Score 79; DB 18; Length 496;
Best Local Similarity 100.0%; Pred. No. 2e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
| | | | | | | | | | | | | | | | | |
Db 189 RHYGETKNQSRSS 203

RESULT 3
US-10-828-985A-11
; Sequence 11, Application US/10828985A
; Publication No. US2005003402A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Christopher D
; APPLICANT: Castle, John C
; APPLICANT: Garrett-Englele, Philip W
; APPLICANT: Kan, Zhengyan
; APPLICANT: Loerch, Patrick M
; APPLICANT: Tsinoresmas, Nicholas F
; TITLE OF INVENTION: Novel Isoforms of Centromere Protein E (CENPE)
; FILE REFERENCE: RS0210Y
; CURRENT APPLICATION NUMBER: US/10/828,985A
; CURRENT FILING DATE: 2004-04-21
; PRIOR APPLICATION NUMBER: US 60/464,905
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 60/510,701
; PRIOR FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 2503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-828-985A-11

Query Match 100.0%; Score 79; DB 17; Length 2503;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
| | | | | | | | | | | | | | | | | |
Db 189 RHYGETKNQSRSS 203

RESULT 4

US-10-828-985A-9
; Sequence 9, Application US/10828985A
; Publication No. US2005003402A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Christopher D
; APPLICANT: Castle, John C
; APPLICANT: Garrett-Englele, Philip W
; APPLICANT: Kan, Zhengyan
; APPLICANT: Loerch, Patrick M
; APPLICANT: Tsinoresmas, Nicholas F
; TITLE OF INVENTION: Novel Isoforms of Centromere Protein E (CENPE)
; FILE REFERENCE: RS0210Y
; CURRENT APPLICATION NUMBER: US/10/828,985A
; CURRENT FILING DATE: 2004-04-21
; PRIOR APPLICATION NUMBER: US 60/464,905
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 60/510,701
; PRIOR FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 2543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-828-985A-9

Query Match 100.0%; Score 79; DB 17; Length 2543;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
| | | | | | | | | | | | | | | | | |
Db 189 RHYGETKNQSRSS 203

RESULT 5
US-10-828-985A-7
; Sequence 7, Application US/10828985A
; Publication No. US2005003402A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Christopher D
; APPLICANT: Castle, John C
; APPLICANT: Garrett-Englele, Philip W
; APPLICANT: Kan, Zhengyan
; APPLICANT: Loerch, Patrick M
; APPLICANT: Tsinoresmas, Nicholas F
; TITLE OF INVENTION: Novel Isoforms of Centromere Protein E (CENPE)
; FILE REFERENCE: RS0210Y
; CURRENT APPLICATION NUMBER: US/10/828,985A
; CURRENT FILING DATE: 2004-04-21
; PRIOR APPLICATION NUMBER: US 60/464,905
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 60/510,701
; PRIOR FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 2568
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-828-985A-7

Query Match 100.0%; Score 79; DB 17; Length 2568;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
| | | | | | | | | | | | | | | | | |
Db 189 RHYGETKNQSRSS 203

RESULT 6
US-10-450-763-36864

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; Sequence 36864, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 36864
; LENGTH: 2633
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (77)..(99)
; OTHER INFORMATION: KINESIN HEAVY CHAIN SIGNATURE domain identified by eMATRIX,
; accession number FR00380A, p-value=1.000e-25, raw score of 14.18
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (12)..(2412)
; OTHER INFORMATION: Kinesin motor domain identified by Pfam, accession name
; OTHER INFORMATION: kinesin, E-value=4.9e-217, Pfam score of 734.4
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2633)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-36864

Query Match 100.0%; Score 79; DB 18; Length 2633;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSRSS 15
Db 189 RHYGETKMNQSRSS 203

RESULT 7
US-10-723-860-749
; Sequence 749, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; METHODS OF SCREENING FOR SOFT TISSUE SARCOMA MODULATORS
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 749
; LENGTH: 2663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-749

Query Match 100.0%; Score 79; DB 16; Length 2663;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSRSS 15
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Db 189 RHYGETKMNQSRSS 203

RESULT 8
US-10-650-280-1
; Sequence 1, Application US/10650280
; Publication No. US20050191631A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Kenneth W.
; APPLICANT: Sakowicz, Roman
; APPLICANT: Goldstein, Lawrence S.B.
; APPLICANT: Cleveland, Don W.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Plus End-Directed Microtubule Motor Required for
; TITLE OF INVENTION: Chromosome Congression
; FILE REFERENCE: 18557C-000110US
; CURRENT APPLICATION NUMBER: US/10/650,280
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/150,867
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,645
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2954
; TYPE: PRT
; ORGANISM: Xenopus sp.
; FEATURE:
; OTHER INFORMATION: Xenopus centromere-associated protein-E (XCENP-E)
; OTHER INFORMATION: member of the kinesin superfamily of microtubule
; OTHER INFORMATION: motor proteins
; NAME/KEY: DOMAIN
; LOCATION: (1)..(472)
; OTHER INFORMATION: kinesin like motor domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (473)..(2752)
; OTHER INFORMATION: rod domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (2753)..(2954)
; OTHER INFORMATION: tail domain
US-10-650-280-1

Query Match 87.3%; Score 69; DB 18; Length 2954;
Best Local Similarity 86.7%; Pred. No. 0.0081;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSRSS 15
Db 187 RHYGETKMNQSRSS 201

RESULT 9
US-10-425-115-263022
; Sequence 263022, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 263022
; LENGTH: 668
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; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_171488C.1.pep
US-10-425-115-263022

Query Match 82.3%; Score 65; DB 16; Length 668;
Best Local Similarity 80.0%; Pred. No. 0.0086;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
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Db 195 RHFGETNMNRSRS 209

RESULT 10
US-10-425-114-59725
; Sequence 59725, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59725
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3912-011-C4_FLI.pep
US-10-425-114-59725

Query Match 82.3%; Score 65; DB 15; Length 694;
Best Local Similarity 80.0%; Pred. No. 0.0089;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
||:|||||
Db 221 RHFGETNMNRSRS 235

RESULT 11
US-10-437-963-116808
; Sequence 116808, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 116808
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_20274C.1.pep
US-10-437-963-116808

Query Match 79.7%; Score 63; DB 16; Length 201;
Best Local Similarity 80.0%; Pred. No. 0.0054;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
||:|||||
Db 41 RHFGETNMNRSRS 55

RESULT 12
US-11-097-143-13758
; Sequence 13758, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,932
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,931
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13758
; LENGTH: 2013
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-13758

Query Match 67.1%; Score 53; DB 20; Length 2013;
Best Local Similarity 73.3%; Pred. No. 3.8;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
||:|||||
Db 183 RTVGETNMNRSRS 197

RESULT 13
US-09-864-408A-1218
; Sequence 1218, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides En
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1218
; LENGTH: 154

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(1)

; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
US-09-864-408A-1218

Query Match 65.8%; Score 52; DB 11; Length 154;
Best Local Similarity 66.7%; Pred. NO. 0.37;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNORSSRS 15

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Db 29 RHTGTTQWNEHSSRS 43

RESULT 14

US-10-437-963-176714

; Sequence 176714, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 176714

; LENGTH: 1382

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_74437C.1.pap

US-10-437-963-176714

Query Match 65.8%; Score 52; DB 16; Length 1382;

Best Local Similarity 73.3%; Pred. NO. 3.9;

Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNORSSRS 15

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Db 180 RHIGETNMVYSSRS 194

RESULT 15

US-10-287-226-142

; Sequence 142, Application US/10287226

; Publication No. US20040086875A1

; GENERAL INFORMATION:

; APPLICANT: Agee, Michele L.,

; APPLICANT: Alsobrook, John P.,

; APPLICANT: Berghs, Constance,

; APPLICANT: Boldog, Ference,

; APPLICANT: Burgess, Catherine E.,

; APPLICANT: Chant, John S.,

; APPLICANT: Chaudhuri, Amitabha,

; APPLICANT: DiPippo, Vincent A.,

; APPLICANT: Edinger, Shlomit R.,

; APPLICANT: Eisen, Andrew,

; APPLICANT: Ellerman, Karen,

; APPLICANT: Gangolli, Esha A.,

; APPLICANT: Gorman, Linda,

; APPLICANT: Gerlach, Valerie,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Khramtsov, Nikolai,
; APPLICANT: Li, Li,
; APPLICANT: Malyankar, Uriel M.,
; APPLICANT: MacDougall, John R.,
; APPLICANT: Mezes, Peter S.,
; APPLICANT: Miller, Charles E.,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Ooi, Chean Eng,
; APPLICANT: Ort, Tatiana,
; APPLICANT: Padigaru, Muralidhara,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rastelli, Luca,
; APPLICANT: Rieger, Daniel K.,
; APPLICANT: Rothenberg, Mark E.,
; APPLICANT: Shenoy, Suresh G.,
; APPLICANT: Spaderna, Steven K.,
; APPLICANT: Spytek, Kimberley A.,
; APPLICANT: Taupier, Jr., Raymond J.,
; APPLICANT: Vernet, Corine A.M.,
; APPLICANT: Zerhusen, Bryan D.,
; APPLICANT: Zhong, Wei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-480C
; CURRENT APPLICATION NUMBER: US/10/287,226
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: 60/334,421
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,392
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/360,148
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/364,227
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/334,027
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; PRIOR FILING DATE: 2001-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 142
; LENGTH: 1401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-226-142

Query Match 65.8%; Score 52; DB 15; Length 1401;

Best Local Similarity 66.7%; Pred. NO. 3.9;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNORSSRS 15

||| |||. |||. |||

Db 193 RHTGTTQWNEHSSRS 207

Search completed: November 1, 2005, 19:07:11

Job time : 168 secs